This Raw Listing contains the General Information Section and up to the first 5 pages.

ENTERED

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 1                                    SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5        (i) APPLICANT: Lobb, Roy R.
 6
 7       (ii) TITLE OF INVENTION: Treatment for Asthma
 8
 9      (iii) NUMBER OF SEQUENCES: 4
10
11       (iv) CORRESPONDENCE ADDRESS:
12            (A) ADDRESSEE: LAHIVE & COCKFIELD
13            (B) STREET: 60 State Street, Suite 510
14            (C) CITY: Boston
15            (D) STATE: Massachusetts
16            (E) COUNTRY: USA
17            (F) ZIP: 02109-1875
18
19        (v) COMPUTER READABLE FORM:
20            (A) MEDIUM TYPE: Floppy disk
21            (B) COMPUTER: IBM PC compatible
22            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
23            (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
24
25       (vi) CURRENT APPLICATION DATA:
26            (A) APPLICATION NUMBER: US 08/256,631
27       (B) FILING DATE: 12-JUL-1994
28
29      (vii) PRIOR APPLICATION DATA:
30            (A) APPLICATION NUMBER: PCT/US93/00030
31            (B) FILING DATE: 12-JAN-1993
32       (C) APPLICATION NUMBER: US 07/821,768
33            (D) FILING DATE: 13-JAN-1992
34
35     (viii) ATTORNEY/AGENT INFORMATION:
36            (A) NAME: Myers, Louis (PLM)
37            (B) REGISTRATION NUMBER: 35,965
38            (C) REFERENCE/DOCKET NUMBER: D002 CIP PCT (BGP-021US)
39
40       (ix) TELECOMMUNICATION INFORMATION:
41            (A) TELEPHONE: (617)227-7400
42            (B) TELEFAX: (617)227-5941
43
44
45   (2) INFORMATION FOR SEQ ID NO:1:
46
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47          (i)  SEQUENCE CHARACTERISTICS:
48               (A)  LENGTH: 360 base pairs
49               (B)  TYPE: nucleic acid
50               (C)  STRANDEDNESS: single
51               (D)  TOPOLOGY: linear
52
53         (ii)  MOLECULE TYPE: cDNA
54
55
56         (ix)  FEATURE:
57               (A)  NAME/KEY: CDS
58               (B)  LOCATION: 1..360
59
60         (ix)  FEATURE:
61               (A)  NAME/KEY: misc_feature
62               (B)  LOCATION: 1
63               (D)  OTHER INFORMATION: /note= "pBAG159 insert: HP1/2 heavy
64                    chain variable region; amino acid 1 is Glu (E) but
65                    Gln (Q) may be substituted"
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70   GTC AAA CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG CCA GGG GCC TCA          48
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72    1               5                  10                  15
73
74   GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT AAA GAC ACC TAT          96
75   Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
76                   20                  25                  30
77
78   ATG CAC TGG GTG AAG CAG AGG CCT GAA CAG GGC CTG GAG TGG ATT GGA          144
79   Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
80                   35                  40                  45
81
82   AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC CCG AAG TTC CAG          192
83   Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
84        50                  55                  60
85
86   GTC AAG GCC ACT ATT ACA GCG GAC ACG TCC TCC AAC ACA GCC TGG CTG          240
87   Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
88    65                  70                  75                  80
89
90   CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAC TAC TGT GCA          288
91   Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
92                   85                  90                  95
93
94   GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC TTC TGG GGC CAA          336
95   Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
96                   100                 105                 110
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98   GGG ACC ACG GTC ACC GTC TCC TCA                                          360
99   Gly Thr Thr Val Thr Val Ser Ser
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106            (A) LENGTH: 120 amino acids
107            (B) TYPE: amino acid
108            (D) TOPOLOGY: linear
109
110        (ii) MOLECULE TYPE: protein
111
112        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
113
114    Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
115     1               5                  10                  15
116
117    Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
118               20                  25                  30
119
120    Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
121           35                  40                  45
122
123    Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
124       50                  55                  60
125
126    Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
127     65                  70                  75                  80
128
129    Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
130               85                  90                  95
131
132    Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
133           100                 105                 110
134
135    Gly Thr Thr Val Thr Val Ser Ser
136           115                 120
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138    (2) INFORMATION FOR SEQ ID NO:3:
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140        (i) SEQUENCE CHARACTERISTICS:
141            (A) LENGTH: 318 base pairs
142            (B) TYPE: nucleic acid
143            (C) STRANDEDNESS: single
144            (D) TOPOLOGY: linear
145
146        (ii) MOLECULE TYPE: cDNA
147
148
149        (ix) FEATURE:
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151            (B) LOCATION: 1..318
152            (D) OTHER INFORMATION: /note= "HP1/2 light chain variable
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INPUT SET: S4634.raw

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153                              region"
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155        (ix) FEATURE:
156             (A) NAME/KEY: misc_feature
157             (B) LOCATION: 1
158             (D) OTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light
159                 chain variable region"
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161
162        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
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164   AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA        48
165   Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
166    1               5                  10                  15
167
168   GAC AGG GTT ACC ATA ACC TGC AAG GCC AGT CAG AGT GTG ACT AAT GAT        96
169   Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
170            20                  25                  30
171
172   GTA GCT TGG TAC CAA CAG AAG CCA GGG CAG TCT CCT AAA CTG CTG ATA       144
173   Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
174            35                  40                  45
175
176   TAT TAT GCA TCC AAT CGC TAC ACT GGA GTC CCT GAT CGC TTC ACT GGC       192
177   Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
178        50                  55                  60
179
180   AGT GGA TAT GGG ACG GAT TTC ACT TTC ACC ATC AGC ACT GTG CAG GCT       240
181   Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
182    65                  70                  75                  80
183
184   GAA GAC CTG GCA GTT TAT TTC TGT CAG CAG GAT TAT AGC TCT CCG TAC       288
185   Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
186                85                  90                  95
187
188   ACG TTC GGA GGG GGG ACC AAG CTG GAG ATC                              318
189   Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
190                100                 105
191
192
193   (2) INFORMATION FOR SEQ ID NO:4:
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195        (i) SEQUENCE CHARACTERISTICS:
196             (A) LENGTH: 106 amino acids
197             (B) TYPE: amino acid
198             (D) TOPOLOGY: linear
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200        (ii) MOLECULE TYPE: protein
201
202        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
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204   Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
205    1               5                  10                  15
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/256,631*

DATE: 07/06/95
TIME: 11:51:02

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213   Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
214       50                  55                  60
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216   Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
217   65                  70                  75                  80
218
219   Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
220                   85                  90                  95
221
222   Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
223           100                 105
224
225
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/256,631*

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